

# SEQUENCE LISTING

<110> Flint, Dennis

Meyer, Knut

Viitanen, Paul

<120> Sinapoylglucose:Malate Sinapoyltransferase Form Malate  
Conjugates From Benzoic Acid Glucosides

<130> BC1034 US NA

<140> US 60/216,615

<141> 2000-07-07

<150> 60/216,615

<151> July 7, 2000

<160> 19

<170> Microsoft Office 97

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<212> PRT

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Asn	Val	Gln	Phe	Phe	Tyr	Tyr	Phe	Ile	Lys	Ser	Glu	Asn	Asn	Pro	Lys
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Leu	Gly	Gly	Ile	Ile 85	Phe	Glu	Asn	Gly	Pro 90	Val	Gly	Leu	Lys	Phe	Glu 95
Val	Phe	Asn	Gly 100	Ser	Ala	Pro	Ser	Leu 105	Phe	Ser	Thr	Thr	Tyr 110	Ser	Trp
Thr	Lys	Met 115	Ala	Asn	Ile	Ile	Phe 120	Leu	Asp	Gln	Pro	Val 125	Gly	Ser	Gly
Phe	Ser 130	Tyr	Ser	Lys	Thr	Pro 135	Ile	Asp	Lys	Thr	Gly 140	Asp	Ile	Ser	Glu
Val 145	Lys	Arg	Thr	His 150	Glu	Phe	Leu	Gln	Lys	Trp 155	Leu	Ser	Arg	His	Pro 160
Gln	Tyr	Phe	Ser	Asn 165	Pro	Leu	Tyr	Val	Val 170	Gly	Asp	Ser	Tyr	Ser	Gly 175
Met	Ile	Val 180	Pro	Ala	Leu	Val	Gln 185	Glu	Ile	Ser	Gln	Gly	Asn 190	Tyr	Ile
Cys	Cys	Glu 195	Pro	Pro	Ile	Asn	Leu 200	Gln	Gly	Tyr	Met	Leu 205	Gly	Asn	Pro
Val 210	Thr	Tyr	Met	Asp	Phe	Glu 215	Gln	Asn	Phe	Arg	Ile 220	Pro	Tyr	Ala	Tyr
Gly 225	Met	Gly	Leu	Ile	Ser	Asp 230	Glu	Ile	Tyr	Glu 235	Pro	Met	Lys	Arg	Ile 240
Cys	Asn	Gly	Asn 245	Tyr	Tyr	Asn	Val	Asp 250	Pro	Ser	Asn	Thr	Gln	Cys 255	Leu
Lys	Leu	Thr	Glu 260	Glu	Tyr	His	Lys	Cys 265	Thr	Ala	Lys	Ile	Asn 270	Ile	His
His	Ile 275	Leu	Thr	Pro	Asp	Cys	Asp 280	Val	Thr	Asn	Val 285	Thr	Ser	Pro	Asp
Cys	Tyr 290	Tyr	Tyr	Pro	Tyr	His 295	Leu	Ile	Glu	Cys	Trp 300	Ala	Asn	Asp	Glu
Ser 305	Val	Arg	Glu	Ala	Leu 310	His	Ile	Glu	Lys	Gly 315	Ser	Lys	Gly	Lys	Trp 320
Ala	Arg	Cys	Asn 325	Arg	Thr	Ile	Pro	Tyr	Asn 330	His	Asp	Ile	Val	Ser	Ser 335
Ile	Pro	Tyr	His 340	Met	Asn	Asn	Ser	Ile 345	Ser	Gly	Tyr	Arg	Ser	Leu	Ile
Tyr	Ser	Gly 355	Asp	His	Asp	Ile	Ala 360	Val	Pro	Phe	Leu	Ala 365	Thr	Gln	Ala
Trp 370	Ile	Arg	Ser	Leu	Asn	Tyr 375	Ser	Pro	Ile	His	Asn 380	Trp	Arg	Pro	Trp
Met 385	Ile	Asn	Asn	Gln	Ile 390	Ala	Gly	Tyr	Thr	Arg 395	Ala	Tyr	Ser	Asn	Lys 400

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tacattggta ttggtgagga cgagaatgtg caatttttct actatttcat caaatctgaa	180
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agtgtcctt ctttgttctc tactacatat tcatggacaa agatggcaaa catttatattc	360
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gacataagtg aagtaaagag gacccatgag tttcttcaaa agtggctaag caggcatcca	480
caatatttct ccaacccttt atatgtagtt ggagattctt attccggtat gattgtcccg	540
gccctcgttc aagaaatctc acaaggaaat tatatatgtt gcgaacctcc tataaatcta	600
cagggttata tgcttgga aa cctgtaaca tatatggact ttgaacaaaa cttccgcatt	660
ccatatgctt atgggatggg attaatctcc gacgaaatct atgagccaat gaagagaatc	720
tgcaacggaa attattacaa tgtggatcca tctaacacac aatgtttgaa acttactgaa	780
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gcgcgatgta atcggactat tccatacaat cacgacattg taagcagcat accatatcac	1020
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gtcccttttc ttgcaactca agcctggata agatctctca attactcccc cattcataac	1140
tggaggccat ggatgataaa caatcaaate gctggataca cgagagctta ttccaataag	1200
atgacatttg ctactatcaa aggaggtgga cacacggcag agtatagacc aaacgagacc	1260

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1302

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<212> DNA

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aatctgaaaa	caatccaaaa	gaagatcctc	ttcttatatg	gttaaattga	ggacctggat	180
gttcttgtct	tggtggtatt	atctttgaga	acggaccggt	gggtttgaag	tttgaggtgt	240
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aaactggtga	cataagtga	gtaaagagga	cccatgagtt	tcttcaaaag	tggctaagca	420
ggcatccaca	atatttctcc	aaccctttat	atgtagttgg	agattcttat	tccggtatga	480
ttgtcccggc	cctcgttcaa	gaaatctcac	aaggaaatta	tatatgttgc	gaacctccta	540
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tccgcattcc	atatgcttat	ggtatgggat	taatctccga	cgaaatctat	gagccaatga	660
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ttactgaaga	atatcataag	tgactgcca	aaataaatat	ccatcacata	ttaacaccag	780
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gaaaatgggc	gcgatgtaat	cggactattc	catacaatca	cgacattgta	agcagcatac	960
catatcacat	gaataacagc	atcagtggat	accgatctct	tatttacagt	ggtgatcacg	1020
acatcgcggt	cccttttctt	gcaactcaag	cctggataag	atctctcaat	tactccccca	1080
ttcataactg	gaggccatgg	atgataaaca	atcaaactgc	tggatacacg	agagcttatt	1140
ccaataagat	gacatttgct	actatcaaag	gaggtggaca	cacggcagag	tatagaccaa	1200
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<212> PRT

<213> Arabidopsis thaliana

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Gln	Phe	Phe	Tyr	Tyr	Phe	Ile	Lys	Ser	Glu	Asn	Asn	Pro	Lys	Glu	Asp	
		35					40					45				
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65					70				75						80	
Asn	Gly	Ser	Ala	Pro	Ser	Leu	Phe	Ser	Thr	Thr	Tyr	Ser	Trp	Thr	Lys	
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Tyr	Ser	Lys	Thr	Pro	Ile	Asp	Lys	Thr	Gly	Asp	Ile	Ser	Glu	Val	Lys	
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Val	Pro	Ala	Leu	Val	Gln	Glu	Ile	Ser	Gln	Gly	Asn	Tyr	Ile	Cys	Cys	
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Tyr	Met	Asp	Phe	Glu	Gln	Asn	Phe	Arg	Ile	Pro	Tyr	Ala	Tyr	Gly	Met	
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Gly	Asn	Tyr	Tyr	Asn	Val	Asp	Pro	Ser	Asn	Thr	Gln	Cys	Leu	Lys	Leu	
225					230					235					240	
Thr	Glu	Glu	Tyr	His	Lys	Cys	Thr	Ala	Lys	Ile	Asn	Ile	His	His	Ile	
				245					250					255		
Leu	Thr	Pro	Asp	Cys	Asp	Val	Thr	Asn	Val	Thr	Ser	Pro	Asp	Cys	Tyr	
			260					265					270			
Tyr	Tyr	Pro	Tyr	His	Leu	Ile	Glu	Cys	Trp	Ala	Asn	Asp	Glu	Ser	Val	
		275					280					285				
Arg	Glu	Ala	Leu	His	Ile	Glu	Lys	Gly	Ser	Lys	Gly	Lys	Trp	Ala	Arg	
	290					295					300					

Cys Asn Arg Thr Ile Pro Tyr Asn His Asp Ile Val Ser Ser Ile Pro  
 305 310 315 320  
 Tyr His Met Asn Asn Ser Ile Ser Gly Tyr Arg Ser Leu Ile Tyr Ser  
 325 330 335  
 Gly Asp His Asp Ile Ala Val Pro Phe Leu Ala Thr Gln Ala Trp Ile  
 340 345 350  
 Arg Ser Leu Asn Tyr Ser Pro Ile His Asn Trp Arg Pro Trp Met Ile  
 355 360 365  
 Asn Asn Gln Ile Ala Gly Tyr Thr Arg Ala Tyr Ser Asn Lys Met Thr  
 370 375 380  
 Phe Ala Thr Ile Lys Gly Gly Gly His Thr Ala Glu Tyr Arg Pro Asn  
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<211> 27

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<221> misc\_feature

<223> primer

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<210> 9

<211> 1317

<212> DNA

<213> Arabidopsis thaliana

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 gaaaccgggt acattggtat tggtaggac gagaatgtgc aatttttcta ctatttcac 180  
 aaatctgaaa acaatccaaa agaagatcct cttcttatat ggttaaattgg aggacctgga 240  
 tgttcttgtc ttggtggtat tatttttgag aacggaccgg tgggttgaa gtttgagggtg 300

ttcaacggaa gtgctccttc tttgttctct actacatatt catggacaaa gatggcaaac	360
attatattct tggatcagcc agtaggatct ggcttctcct actcaaaaac tccaattgat	420
aaaactggtg acataagtga agtaaagagg acccatgagt ttcttcaaaa gtggctaagc	480
aggcatccac aatatttctc caacccttta tatgtagttg gagattctta ttccggtatg	540
attgtcccgg ccctcgttca agaaatctca caaggaaatt atatatgttg cgaacctcct	600
ataaatctac agggttatat gcttggaac cctgtaacat atatggactt tgaacaaaac	660
ttccgcattc catatgctta tggatatgga ttaatctccg acgaaatcta tgagccaatg	720
aagagaatct gcaacggaaa ttattacaat gtggatccat ctaacacaca atgtttgaaa	780
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gattgcatg taaccaatgt aacatctcct gattgttatt attatccata tcatctcatt	900
gaatgttggg ctaacgacga gagcggtcgc gaagctcttc atattgaaaa gggtagtaaa	960
ggaaaatggg cgcatgtaa tcggactatt ccatacaatc acgacattgt aagcagcata	1020
ccatatcaca tgaataacag catcagtgga taccgatctc ttatttacag tggatgacac	1080
gacatcgcg tcccttttct tgcaactcaa gcctggataa gatctctcaa ttactcccc	1140
attcataact ggaggccatg gatgataaac aatcaaatcg ctggatacac gagagcttat	1200
tccaataaga tgacatttgc tactatcaaa ggaggtggac acacggcaga gtatagacca	1260
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 cagcagggaa aaacggtaag cgtgacgatg atccgcgaag ggtttgctga gcagaatgaa 180  
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 ttatgtgccg atggtgaacc gtggcttgcc ggtcgtagcg tcgttcctgt gtcaacgtta 300  
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 acatcatcga cattaaccg ggactttatt gagataggcc gtgatgccgg gctgtggggg 420  
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 Asp Ser Met Thr Lys Arg Phe Glu Gln Gln Gly Lys Thr Val Ser Val  
                   35                  40                  45  
 Thr Met Ile Arg Glu Gly Phe Val Glu Gln Asn Glu Ile Pro Glu Glu  
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 Leu Pro Leu Leu Pro Lys Glu Ser Arg Tyr Trp Leu Arg Glu Ile Leu  
   65                  70                  75                  80  
 Leu Cys Ala Asp Gly Glu Pro Trp Leu Ala Gly Arg Thr Val Val Pro  
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 Val Ser Thr Leu Ser Gly Pro Glu Leu Ala Leu Gln Lys Leu Gly Lys  
                  100                 105                 110  
 Thr Pro Leu Gly Arg Tyr Leu Phe Thr Ser Ser Thr Leu Thr Arg Asp  
           115                 120                 125  
 Phe Ile Glu Ile Gly Arg Asp Ala Gly Leu Trp Gly Arg Arg Ser Arg  
   130                 135                 140  
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<211> 32

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<221> misc\_feature

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<223> open reading frame of the chloroplast-targeted CPL fusion protein

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caaaaccttg acatcacttc cattgctagc aatgggtggaa gagttagctg catgcaggtg 180

tggcatatgt cacacccgc gttaacgcaa ctgcgtgctg tgcgctattg taaagagatc 240

cctgccctgg atccgcaact gctcgactgg ctggtgctgg aggattccat gacaaaacgt 300

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acgttaagcg ggccggagct ggcgttacaa aaattgggta aaacgccgtt aggacgctat 540

ctgttcacat catcgacatt aaccggggac ttatttgaga taggccgtga tgccgggctg 600

tgggggagac gttccgcct gcgattaagc ggtaaaccgc tgttgctaac agaactgttt 660

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<213> Artificial Sequence

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<222> (1)..(227)

<223> open reading frame of the chloroplast-targeted CPL fusion protein

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			20					25					30		
Ala	Thr	Phe	Pro	Val	Thr	Lys	Lys	Gln	Asn	Leu	Asp	Ile	Thr	Ser	Ile
		35					40					45			
Ala	Ser	Asn	Gly	Gly	Arg	Val	Ser	Cys	Met	Gln	Val	Trp	His	Met	Ser
	50					55					60				
His	Pro	Ala	Leu	Thr	Gln	Leu	Arg	Ala	Leu	Arg	Tyr	Cys	Lys	Glu	Ile
65					70					75				80	
Pro	Ala	Leu	Asp	Pro	Gln	Leu	Leu	Asp	Trp	Leu	Leu	Leu	Glu	Asp	Ser
				85					90					95	
Met	Thr	Lys	Arg	Phe	Glu	Gln	Gln	Gly	Lys	Thr	Val	Ser	Val	Thr	Met
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Ile	Arg	Glu	Gly	Phe	Val	Glu	Gln	Asn	Glu	Ile	Pro	Glu	Glu	Leu	Pro
		115					120					125			
Leu	Leu	Pro	Lys	Glu	Ser	Arg	Tyr	Trp	Leu	Arg	Glu	Ile	Leu	Leu	Cys
	130					135					140				
Ala	Asp	Gly	Glu	Pro	Trp	Leu	Ala	Gly	Arg	Thr	Val	Val	Pro	Val	Ser
145					150					155					160
Thr	Leu	Ser	Gly	Pro	Glu	Leu	Ala	Leu	Gln	Lys	Leu	Gly	Lys	Thr	Pro
				165					170					175	
Leu	Gly	Arg	Tyr	Leu	Phe	Thr	Ser	Ser	Thr	Leu	Thr	Arg	Asp	Phe	Ile
			180					185					190		
Glu	Ile	Gly	Arg	Asp	Ala	Gly	Leu	Trp	Gly	Arg	Arg	Ser	Arg	Leu	Arg
		195					200					205			
Leu	Ser	Gly	Lys	Pro	Leu	Leu	Leu	Thr	Glu	Leu	Phe	Leu	Pro	Ala	Ser
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<213> Artificial Sequence

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<400> 18

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34